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1643

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/498,098DATE: 05/19/2000
TIME: 18:57:21

Input Set: I498098.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Stack, Jeffrey H.
2 Whitney, Michael
3 Cubitt, Andrew B.
4 Pollok, Brian A.
5 <120> TITLE OF INVENTION: METHODS OF PROTEIN DESTABILIZATION AND
6 USES THEREOF
7 <130> FILE REFERENCE: AURO1330
8 <140> CURRENT APPLICATION NUMBER: US/09/498,098
9 <141> CURRENT FILING DATE: 2000-02-04
10 <160> NUMBER OF SEQ ID NOS: 74
11 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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15 <213> ORGANISM: Eukaryote
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17 <221> NAME/KEY: VARIANT
18 <222> LOCATION: 2, 6
19 <223> OTHER INFORMATION: Phosphoserine
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cagaggttga tccttgctgg gaaacagctg gaagatggac gcacctgtc tgactacaac 180
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31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)...(795)
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35 1 5 10 15
36 ttg ggt gca cga gtg ggt tac atc gaa ctg gat ctc aac aac ggt aag 96

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45 Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys
 46 20 25 30
 47 atc ctt gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg agc act 144
 48 Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr
 49 35 40 45
 50 ttt aaa gtt ctg cta tgt ggc gcg gta tta tcc cgt gtt gac gcc ggg 192
 51 Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly
 52 50 55 60
 53 caa gag caa ctc ggt cgc cgc ata cac tat tct cag aat gac ttg gtt 240
 54 Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val
 55 65 70 75 80
 56 gag tac tca cca gtc aca gaa aag cat ctt acg gat ggc atg aca gta 288
 57 Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val
 58 85 90 95
 59 aga gaa tta tgc agt gct gcc ata acc atg agt gat aac act gcg gcc 336
 60 Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala
 61 100 105 110
 62 aac tta ctt ctg aca acg atc gga gga ccg aag gag cta acc gct ttt 384
 63 Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe
 64 115 120 125
 65 ttg cac aac atg ggg gat cat gta act cgc ctt gat cgt tgg gaa ccg 432
 66 Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro
 67 130 135 140
 68 gag ctg aat gaa gcc ata cca aac gac gag cgt gac acc acg atg cct 480
 69 Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro
 70 145 150 155 160
 71 gca gca atg gca aca acg ttg cgc aaa cta tta act ggc gaa cta ctt 528
 72 Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu
 73 165 170 175
 74 act cta gct tcc cgg caa caa tta ata gac tgg atg gag gcg gat aaa 576
 75 Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys
 76 180 185 190
 77 gtt gca gga cca ctt ctg cgc tcg gcc ctt ccg gct ggc tgg ttt att 624
 78 Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile
 79 195 200 205
 80 gct gat aaa tct gga gcc ggt gag cgt ggg tct cgc ggt atc att gca 672
 81 Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala
 82 210 215 220
 83 gca ctg ggg cca gat ggt aag ccc tcc cgt atc gta gtt atc tac acg 720
 84 Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr
 85 225 230 235 240
 86 acg ggg agt cag gca act atg gat gaa cga aat aga cag atc gct gag 768
 87 Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu
 88 245 250 255
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 90 Ile Gly Ala Ser Leu Ile Lys His Trp
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 92 <210> SEQ ID NO 4
 93 <211> LENGTH: 858
 94 <212> TYPE: DNA

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Phe Cys Leu Pro Val Phe Gly His Pro Glu Thr Leu Val Lys Val Lys	
20 25 30	
gat gct gaa gat cag ttg ggt gca cga gtg ggt tac atc gaa ctg gat	144
Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp	
35 40 45	
ctc aac agc ggt aag atc ctt gag agt ttt cgc ccc gaa gaa cgt ttt	192
Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe	
50 55 60	
cca atg atg agc act ttt aaa gtt ctg cta tgt ggc gcg gta tta tcc	240
Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser	
65 70 75 80	
cgt gtt gac gcc ggg caa gag caa ctc ggt cgc cgc ata cac tat tct	288
Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser	
85 90 95	
cag aat gac ttg gtt gag tac tca cca gtc aca gaa aag cat ctt acg	336
Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr	
100 105 110	
gat ggc atg aca gta aga gaa tta tgc agt gct gcc ata acc atg agt	384
Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser	
115 120 125	
gat aac act gcg gcc aac tta ctt ctg aca acg atc gga gga ccg aag	432
Asp Asn Thr Ala Ala Asn Leu Leu Thr Thr Ile Gly Gly Pro Lys	
130 135 140	
gag cta acc gct ttt ttg cac aac atg ggg gat cat gta act cgc ctt	480
Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu	
145 150 155 160	
gat cgt tgg gaa ccg gag ctg aat gaa gcc ata cca aac gac gag cgt	528
Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg	
165 170 175	
gac acc acg atg cct gca gca atg gca aca acg ttg cgc aaa cta tta	576
Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu	
180 185 190	
act ggc gaa cta ctt act cta gct tcc cgg caa caa tta ata gac tgg	624
Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp	
195 200 205	
atg gag gcg gat aaa gtt gca gga cca ctt ctg cgc tcg gcc ctt ccg	672
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210 215 220	
gct ggc tgg ttt att gct gat aaa tct gga gcc ggt gag cgt ggg tct	720
Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser	

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147	Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile				
148	245	250	255		
149	gta gtt atc tac acg acg ggg agt cag gca act atg gat gaa cga aat				816
150	Val Val Ile Tyr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn				
151	260	265	270		
152	aga cag atc gct gag ata ggt gcc tca ctg att aag cat tgg				858
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157	<212> TYPE: DNA				
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166	1 5 10 15				
167	ttg ggt gca cga gtg ggt tac atc gaa ctg gat ctc aac agc ggt aag				96
168	Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys				
169	20 25 30				
170	atc ctt gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg agc act				144
171	Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr				
172	35 40 45				
173	ttt aaa gtt ctg cta tgt ggc gcg gta tta tcc cgt gat gac gcc ggg				192
174	Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Asp Asp Ala Gly				
175	50 55 60				
176	caa gag caa ctc ggt cgc cgc ata cac tat tct cag aat gac ttg gtt				240
177	Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val				
178	65 70 75 80				
179	gag tac tca cca gtc aca gaa aag cat ctt acg gat ggc atg aca gta				288
180	Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val				
181	85 90 95				
182	aga gaa tta tgc agt gct gcc ata acc atg agt gat aac act gcg gcc				336
183	Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala				
184	100 105 110				
185	aac tta ctt ctg aca acg atc gga gga ccg aag gag cta acc gct ttt				384
186	Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe				
187	115 120 125				
188	ttg cac aac atg ggg gat cat gta act cgc ctt gat cat tgg gaa ccg				432
189	Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp His Trp Glu Pro				
190	130 135 140				
191	gag ctg aat gaa gcc ata cca aac gac gag cgt gac acc acg atg cct				480
192	Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro				
193	145 150 155 160				
194	gta gca atg gca aca acg ttg cgc aaa cta tta act ggc gaa cta ctt				528

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195 Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu
 196 165 170 175
 197 act cta gct tcc cg^g caa caa tta ata gac tgg atg gag g^c gat aaa 576
 198 Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys
 199 180 185 190
 200 gtt gca gga cca ctt ctg cgc tcg gcc ctt cc^g gct ggc tgg ttt att 624
 201 Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile
 202 195 200 205
 203 gct gat aaa tct gga gcc ggt gag cgt ggg tct cgc ggt atc att gca 672
 204 Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala
 205 210 215 220
 206 gca ctg ggg cca gat ggt aag ccc tcc cgt atc gta gtt atc tac acg 720
 207 Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr
 208 225 230 235 240
 209 acg ggg agt cag gca act atg gat gaa cga aat aga cag atc gct gag 768
 210 Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu
 211 245 250 255
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 228 Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile
 229 20 25 30
 230 ctt gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg agc act ttt 144
 231 Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe
 232 35 40 45
 233 aaa gtt ctg cta tgt ggc g^c gta tta tcc cgt att gac gcc ggg caa 192
 234 Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln
 235 50 55 60
 236 gag caa ctc ggt cgc cgc ata cac tat tct cag aat gac ttg gtt gag 240
 237 Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu
 238 65 70 75 80
 239 tac tca cca gtc aca gaa aag cat ctt acg gat ggc atg aca gta aga 288
 240 Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg
 241 85 90 95
 242 gaa tta tgc agt gct gcc ata acc atg agt gat aac act g^c g^c aac 336
 243 Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn
 244 100 105 110

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
